



SEQUENCE LISTING

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Rigel Pharmaceuticals, Inc.

<120> SAK: Modulation of Cellular Proliferation for
Treatment of Cancer

<130> 021044-001210US

<140> US 10/026,021

<141> 2001-12-21

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<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 2913

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2913)

<223> human SAK serine/threonine kinase

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ctg ctt ggt aaa gga tca ttt gct ggt gtc tac aga gct gag tcc att 96
Leu Leu Gly Lys Gly Ser Phe Ala Gly Val Tyr Arg Ala Glu Ser Ile
20 25 30

cac act ggt ttg gaa gtt gca atc aaa atg ata gat aag aaa gcc atg 144
His Thr Gly Leu Glu Val Ala Ile Lys Met Ile Asp Lys Lys Ala Met
35 40 45

tac aaa gca gga atg gta cag aga gtc caa aat gag gtg aaa ata cat 192
Tyr Lys Ala Gly Met Val Gln Arg Val Gln Asn Glu Val Lys Ile His
50 55 60

tgc caa ttg aaa cat cct tct atc ttg gag ctt tat aac tat ttt gaa 240
Cys Gln Leu Lys His Pro Ser Ile Leu Glu Leu Tyr Asn Tyr Phe Glu
65 70 75 80

gat agc aat tat gtg tat ctg gta tta gaa atg tgc cat aat gga gaa 288
Asp Ser Asn Tyr Val Tyr Leu Val Leu Glu Met Cys His Asn Gly Glu
85 90 95

atg aac agg tat cta aag aat aga gtg aaa ccc ttc tca gaa aat gaa 336
Met Asn Arg Tyr Leu Lys Asn Arg Val Lys Pro Phe Ser Glu Asn Glu
100 105 110

gct cga cac ttc atg cac cag atc atc aca ggg atg ttg tat ctt cat 384
Ala Arg His Phe Met His Gln Ile Ile Thr Gly Met Leu Tyr Leu His
115 120 125

tct cat ggt ata cta cac cgg gac ctc aca ctt tct aac ctc cta ctg 432
Ser His Gly Ile Leu His Arg Asp Leu Thr Leu Ser Asn Leu Leu Leu
130 135 140

act cgt aat atg aac atc aag att gct gat ttt ggg ctg gca act caa 480
Thr Arg Asn Met Asn Ile Lys Ile Ala Asp Phe Gly Leu Ala Thr Gln
145 150 155 160

ctg aaa atg cca cat gaa aag cac tat aca tta tgt gga act cct aac 528
Leu Lys Met Pro His Glu Lys His Tyr Thr Leu Cys Gly Thr Pro Asn
165 170 175

tac att tca cca gaa att gcc act cga agt gca cat ggc ctt gaa tct 576
Tyr Ile Ser Pro Glu Ile Ala Thr Arg Ser Ala His Gly Leu Glu Ser
180 185 190

gat gtt tgg tcc ctg ggc tgt atg ttt tat aca tta ctt atc ggg aga 624
Asp Val Trp Ser Leu Gly Cys Met Phe Tyr Thr Leu Leu Ile Gly Arg
195 200 205

cca ccc ttc gac act gac aca gtc aag aac aca tta aat aaa gta gta 672
Pro Pro Phe Asp Thr Asp Thr Val Lys Asn Thr Leu Asn Lys Val Val
210 215 220

ttg gca gat tat gaa atg cca tct ttt ttg tca ata gag gcc aag gac 720
Leu Ala Asp Tyr Glu Met Pro Ser Phe Leu Ser Ile Glu Ala Lys Asp
225 230 235 240

ctt att cac cag tta ctt cgt aga aat cca gca gat cgt tta agt ctg 768
Leu Ile His Gln Leu Leu Arg Arg Asn Pro Ala Asp Arg Leu Ser Leu
245 250 255

tct tca gta ttg gac cat cct ttt atg tcc cga aat tct tca aca aaa 816
Ser Ser Val Leu Asp His Pro Phe Met Ser Arg Asn Ser Ser Thr Lys
260 265 270

agt aaa gat tta gga act gtg gaa gac tca att gat agt ggg cat gcc 864
Ser Lys Asp Leu Gly Thr Val Glu Asp Ser Ile Asp Ser Gly His Ala
275 280 285

aca att tct act gca att aca gct tct tcc agt acc agt ata agt ggt 912
Thr Ile Ser Thr Ala Ile Thr Ala Ser Ser Ser Thr Ser Ile Ser Gly
290 295 300

agt tta ttt gac aaa aga aga ctt ttg att ggt cag cca ctc cca aat 960
Ser Leu Phe Asp Lys Arg Arg Leu Leu Ile Gly Gln Pro Leu Pro Asn
305 310 315 320

aaa atg act gta ttt cca aag aat aaa agt tca act gat ttt tct tct 1008
Lys Met Thr Val Phe Pro Lys Asn Lys Ser Ser Thr Asp Phe Ser Ser
325 330 335

tca gga gat gga aac agt ttt tat act cag tgg gga aat caa gaa acc 1056
Ser Gly Asp Gly Asn Ser Phe Tyr Thr Gln Trp Gly Asn Gln Glu Thr
340 345 350

agt aat agt gga agg gga aga gta att caa gat gca gaa gaa agg cca 1104
 Ser Asn Ser Gly Arg Gly Arg Val Ile Gln Asp Ala Glu Glu Arg Pro
 355 360 365

cat tct cga tac ctt cgt aga gct tat tcc tct gat aga tct ggc act 1152
 His Ser Arg Tyr Leu Arg Arg Ala Tyr Ser Ser Asp Arg Ser Gly Thr
 370 375 380

tct aat agt cag tct caa gca aaa aca tat aca atg gaa cga tgt cac 1200
 Ser Asn Ser Gln Ser Gln Ala Lys Thr Tyr Thr Met Glu Arg Cys His
 385 390 395 400

tca gca gaa atg ctt tca gtg tcc aaa aga tca gga gga ggt gaa aat 1248
 Ser Ala Glu Met Leu Ser Val Ser Lys Arg Ser Gly Gly Gly Glu Asn
 405 410 415

gaa gag agg tac tca ccc aca gac aac aat gcc aac att ttt aac ttc 1296
 Glu Glu Arg Tyr Ser Pro Thr Asp Asn Asn Ala Asn Ile Phe Asn Phe
 420 425 430

ttt aaa gaa aag aca tcc agt agt tct gga tct ttt gaa aga cct gat 1344
 Phe Lys Glu Lys Thr Ser Ser Ser Ser Gly Ser Phe Glu Arg Pro Asp
 435 440 445

aac aat caa gca ctc tcc aat cat ctt tgt cca gga aaa act cct ttt 1392
 Asn Asn Gln Ala Leu Ser Asn His Leu Cys Pro Gly Lys Thr Pro Phe
 450 455 460

cca ttt gca gac ccg aca cct cag act gaa acc gta caa cag tgg ttt 1440
 Pro Phe Ala Asp Pro Thr Pro Gln Thr Glu Thr Val Gln Gln Trp Phe
 465 470 475 480

ggg aat ctg caa ata aat gct cat tta aga aaa act act gaa tat gac 1488
 Gly Asn Leu Gln Ile Asn Ala His Leu Arg Lys Thr Thr Glu Tyr Asp
 485 490 495

agc atc agc cca aac cgg gac ttc cag ggc cat cca gat ttg cag aag 1536
 Ser Ile Ser Pro Asn Arg Asp Phe Gln Gly His Pro Asp Leu Gln Lys
 500 505 510

gac aca tca aaa aat gcc tgg act gat aca aaa gtc aaa aag aac tct 1584
 Asp Thr Ser Lys Asn Ala Trp Thr Asp Thr Lys Val Lys Lys Asn Ser
 515 520 525

gat gct tct gat aat gca cat tct gta aaa cag caa aat acc atg aaa 1632
 Asp Ala Ser Asp Asn Ala His Ser Val Lys Gln Gln Asn Thr Met Lys
 530 535 540

tat atg act gca ctt cac agt aaa cct gag ata atc caa caa gaa tgt 1680
 Tyr Met Thr Ala Leu His Ser Lys Pro Glu Ile Ile Gln Gln Glu Cys
 545 550 555 560

gtt ttt ggc tca gat cct ctt tct gaa cag agc aag act agg ggt atg 1728
 Val Phe Gly Ser Asp Pro Leu Ser Glu Gln Ser Lys Thr Arg Gly Met
 565 570 575

gag cca cca tgg ggt tat cag aat cgt aca tta aga agc att aca tct 1776
 Glu Pro Pro Trp Gly Tyr Gln Asn Arg Thr Leu Arg Ser Ile Thr Ser
 580 585 590

ccg ttg gtt gct cac agg tta aaa cca atc aga cag aaa acc aaa aag 1824
 Pro Leu Val Ala His Arg Leu Lys Pro Ile Arg Gln Lys Thr Lys Lys
 595 600 605

gct gtg gtg agc ata ctt gat tca gag gag gtg tgt gtg gag ctt gta 1872
 Ala Val Val Ser Ile Leu Asp Ser Glu Glu Val Cys Val Glu Leu Val
 610 615 620

aag gag tat gca tct caa gaa tat gtg aaa gaa gtt ctt cag ata tct 1920
 Lys Glu Tyr Ala Ser Gln Glu Tyr Val Lys Glu Val Leu Gln Ile Ser
 625 630 635 640

agt gat gga aat acg atc act att tat tat cca aat ggt ggt aga ggt 1968
 Ser Asp Gly Asn Thr Ile Thr Ile Tyr Tyr Pro Asn Gly Gly Arg Gly
 645 650 655

ttt cct ctt gct gat aga cca ccc tca cct act gac aac atc agt agg 2016
 Phe Pro Leu Ala Asp Arg Pro Pro Ser Pro Thr Asp Asn Ile Ser Arg
 660 665 670

tac agc ttt gac aat tta cca gaa aaa tac tgg cga aaa tat caa tat 2064
 Tyr Ser Phe Asp Asn Leu Pro Glu Lys Tyr Trp Arg Lys Tyr Gln Tyr
 675 680 685

gct tcc agg ttt gta cag ctt gta aga tct aaa tct ccc aaa atc act 2112
 Ala Ser Arg Phe Val Gln Leu Val Arg Ser Lys Ser Pro Lys Ile Thr
 690 695 700

tat ttt aca aga tat gct aaa tgc att ttg atg gag aat tct cct ggt 2160
 Tyr Phe Thr Arg Tyr Ala Lys Cys Ile Leu Met Glu Asn Ser Pro Gly
 705 710 715 720

gct gat ttt gag gtt tgg ttt tat gat ggg gta aaa ata cac aaa aca 2208
 Ala Asp Phe Glu Val Trp Phe Tyr Asp Gly Val Lys Ile His Lys Thr
 725 730 735

gaa gat ttc att cag gtg att gaa aag aca ggg aag tct tac act tta 2256
 Glu Asp Phe Ile Gln Val Ile Glu Lys Thr Gly Lys Ser Tyr Thr Leu
 740 745 750

aaa agt gaa agt gaa gtt aat agc ttg aaa gag gag ata aaa atg tat 2304
 Lys Ser Glu Ser Glu Val Asn Ser Leu Lys Glu Glu Ile Lys Met Tyr
 755 760 765

atg gac cat gct aat gag ggt cat cgt att tgt tta gca ctg gaa tcc 2352
 Met Asp His Ala Asn Glu Gly His Arg Ile Cys Leu Ala Leu Glu Ser
 770 775 780

ata att tca gaa gag gaa agg aaa act agg agt gct ccc ttt ttc cca 2400
 Ile Ile Ser Glu Glu Glu Arg Lys Thr Arg Ser Ala Pro Phe Phe Pro
 785 790 795 800

ata atc ata gga aga aaa cct ggt agt act agt tca cct aag gcc tta 2448
 Ile Ile Ile Gly Arg Lys Pro Gly Ser Thr Ser Ser Pro Lys Ala Leu
 805 810 815

tca cct cct cct tct gtg gat tca aat tac cca acg aga gat aga gca 2496
 Ser Pro Pro Pro Ser Val Asp Ser Asn Tyr Pro Thr Arg Asp Arg Ala
 820 825 830

tct ttc aac aga atg gtc atg cat agt gct gct tct cca aca cag gca 2544
Ser Phe Asn Arg Met Val Met His Ser Ala Ala Ser Pro Thr Gln Ala
835 840 845
cca atc ctt aat ccc tct atg gtt aca aat gaa gga ctt ggt ctt aca 2592
Pro Ile Leu Asn Pro Ser Met Val Thr Asn Glu Gly Leu Gly Leu Thr
850 855 860
act aca gct tct gga aca gac atc tct tct aat agt cta aaa gat tgt 2640
Thr Thr Ala Ser Gly Thr Asp Ile Ser Ser Asn Ser Leu Lys Asp Cys
865 870 875 880
ctt cct aaa tca gca caa ctt ttg aaa tct gtt ttt gtg aaa aat gtt 2688
Leu Pro Lys Ser Ala Gln Leu Leu Lys Ser Val Phe Val Lys Asn Val
885 890 895
ggg tgg gct aca cag tta act agt gga gct gtg tgg gtt cag ttt aat 2736
Gly Trp Ala Thr Gln Leu Thr Ser Gly Ala Val Trp Val Gln Phe Asn
900 905 910
gat ggg tcc cag ttg gtt gtg cag gca gga gtg tct tct atc agt tat 2784
Asp Gly Ser Gln Leu Val Val Gln Ala Gly Val Ser Ser Ile Ser Tyr
915 920 925
acc tca cca aat ggt caa aca act agg tat gga gaa aat gaa aaa tta 2832
Thr Ser Pro Asn Gly Gln Thr Thr Arg Tyr Gly Glu Asn Glu Lys Leu
930 935 940
cca gac tac atc aaa cag aaa tta cag tgt ctg tct tcc atc ctt ttg 2880
Pro Asp Tyr Ile Lys Gln Lys Leu Gln Cys Leu Ser Ser Ile Leu Leu
945 950 955 960
atg ttt tct aat ccg act cct aat ttt cat tga 2913
Met Phe Ser Asn Pro Thr Pro Asn Phe His
965 970

<210> 2

<211> 970

<212> PRT

<213> Homo sapiens

<220>

<223> human SAK serine/threonine kinase

<400> 2

Met Ala Thr Cys Ile Gly Glu Lys Ile Glu Asp Phe Lys Val Gly Asn
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Leu Leu Gly Lys Gly Ser Phe Ala Gly Val Tyr Arg Ala Glu Ser Ile
20 25 30
His Thr Gly Leu Glu Val Ala Ile Lys Met Ile Asp Lys Lys Ala Met
35 40 45
Tyr Lys Ala Gly Met Val Gln Arg Val Gln Asn Glu Val Lys Ile His
50 55 60
Cys Gln Leu Lys His Pro Ser Ile Leu Glu Leu Tyr Asn Tyr Phe Glu
65 70 75 80
Asp Ser Asn Tyr Val Tyr Leu Val Leu Glu Met Cys His Asn Gly Glu
85 90 95
Met Asn Arg Tyr Leu Lys Asn Arg Val Lys Pro Phe Ser Glu Asn Glu
100 105 110

Ala Arg His Phe Met His Gln Ile Ile Thr Gly Met Leu Tyr Leu His
 115 120 125
 Ser His Gly Ile Leu His Arg Asp Leu Thr Leu Ser Asn Leu Leu Leu
 130 135 140
 Thr Arg Asn Met Asn Ile Lys Ile Ala Asp Phe Gly Leu Ala Thr Gln
 145 150 155 160
 Leu Lys Met Pro His Glu Lys His Tyr Thr Leu Cys Gly Thr Pro Asn
 165 170 175
 Tyr Ile Ser Pro Glu Ile Ala Thr Arg Ser Ala His Gly Leu Glu Ser
 180 185 190
 Asp Val Trp Ser Leu Gly Cys Met Phe Tyr Thr Leu Leu Ile Gly Arg
 195 200 205
 Pro Pro Phe Asp Thr Asp Thr Val Lys Asn Thr Leu Asn Lys Val Val
 210 215 220
 Leu Ala Asp Tyr Glu Met Pro Ser Phe Leu Ser Ile Glu Ala Lys Asp
 225 230 235 240
 Leu Ile His Gln Leu Leu Arg Arg Asn Pro Ala Asp Arg Leu Ser Leu
 245 250 255
 Ser Ser Val Leu Asp His Pro Phe Met Ser Arg Asn Ser Ser Thr Lys
 260 265 270
 Ser Lys Asp Leu Gly Thr Val Glu Asp Ser Ile Asp Ser Gly His Ala
 275 280 285
 Thr Ile Ser Thr Ala Ile Thr Ala Ser Ser Ser Thr Ser Ile Ser Gly
 290 295 300
 Ser Leu Phe Asp Lys Arg Arg Leu Leu Ile Gly Gln Pro Leu Pro Asn
 305 310 315 320
 Lys Met Thr Val Phe Pro Lys Asn Lys Ser Ser Thr Asp Phe Ser Ser
 325 330 335
 Ser Gly Asp Gly Asn Ser Phe Tyr Thr Gln Trp Gly Asn Gln Glu Thr
 340 345 350
 Ser Asn Ser Gly Arg Gly Arg Val Ile Gln Asp Ala Glu Glu Arg Pro
 355 360 365
 His Ser Arg Tyr Leu Arg Arg Ala Tyr Ser Ser Asp Arg Ser Gly Thr
 370 375 380
 Ser Asn Ser Gln Ser Gln Ala Lys Thr Tyr Thr Met Glu Arg Cys His
 385 390 395 400
 Ser Ala Glu Met Leu Ser Val Ser Lys Arg Ser Gly Gly Gly Glu Asn
 405 410 415
 Glu Glu Arg Tyr Ser Pro Thr Asp Asn Ala Asn Ile Phe Asn Phe
 420 425 430
 Phe Lys Glu Lys Thr Ser Ser Ser Ser Gly Ser Phe Glu Arg Pro Asp
 435 440 445
 Asn Asn Gln Ala Leu Ser Asn His Leu Cys Pro Gly Lys Thr Pro Phe
 450 455 460
 Pro Phe Ala Asp Pro Thr Pro Gln Thr Glu Thr Val Gln Gln Trp Phe
 465 470 475 480
 Gly Asn Leu Gln Ile Asn Ala His Leu Arg Lys Thr Thr Glu Tyr Asp
 485 490 495
 Ser Ile Ser Pro Asn Arg Asp Phe Gln Gly His Pro Asp Leu Gln Lys
 500 505 510
 Asp Thr Ser Lys Asn Ala Trp Thr Asp Thr Lys Val Lys Lys Asn Ser
 515 520 525
 Asp Ala Ser Asp Asn Ala His Ser Val Lys Gln Gln Asn Thr Met Lys
 530 535 540
 Tyr Met Thr Ala Leu His Ser Lys Pro Glu Ile Ile Gln Gln Glu Cys
 545 550 555 560
 Val Phe Gly Ser Asp Pro Leu Ser Glu Gln Ser Lys Thr Arg Gly Met
 565 570 575
 Glu Pro Pro Trp Gly Tyr Gln Asn Arg Thr Leu Arg Ser Ile Thr Ser
 580 585 590

Pro Leu Val Ala His Arg Leu Lys Pro Ile Arg Gln Lys Thr Lys Lys
 595 600 605
 Ala Val Val Ser Ile Leu Asp Ser Glu Glu Val Cys Val Glu Leu Val
 610 615 620
 Lys Glu Tyr Ala Ser Gln Glu Tyr Val Lys Glu Val Leu Gln Ile Ser
 625 630 635 640
 Ser Asp Gly Asn Thr Ile Thr Ile Tyr Tyr Pro Asn Gly Gly Arg Gly
 645 650 655
 Phe Pro Leu Ala Asp Arg Pro Pro Ser Pro Thr Asp Asn Ile Ser Arg
 660 665 670
 Tyr Ser Phe Asp Asn Leu Pro Glu Lys Tyr Trp Arg Lys Tyr Gln Tyr
 675 680 685
 Ala Ser Arg Phe Val Gln Leu Val Arg Ser Lys Ser Pro Lys Ile Thr
 690 695 700
 Tyr Phe Thr Arg Tyr Ala Lys Cys Ile Leu Met Glu Asn Ser Pro Gly
 705 710 715 720
 Ala Asp Phe Glu Val Trp Phe Tyr Asp Gly Val Lys Ile His Lys Thr
 725 730 735
 Glu Asp Phe Ile Gln Val Ile Glu Lys Thr Gly Lys Ser Tyr Thr Leu
 740 745 750
 Lys Ser Glu Ser Glu Val Asn Ser Leu Lys Glu Glu Ile Lys Met Tyr
 755 760 765
 Met Asp His Ala Asn Glu Gly His Arg Ile Cys Leu Ala Leu Glu Ser
 770 775 780
 Ile Ile Ser Glu Glu Glu Arg Lys Thr Arg Ser Ala Pro Phe Phe Pro
 785 790 795 800
 Ile Ile Ile Gly Arg Lys Pro Gly Ser Thr Ser Ser Pro Lys Ala Leu
 805 810 815
 Ser Pro Pro Pro Ser Val Asp Ser Asn Tyr Pro Thr Arg Asp Arg Ala
 820 825 830
 Ser Phe Asn Arg Met Val Met His Ser Ala Ala Ser Pro Thr Gln Ala
 835 840 845
 Pro Ile Leu Asn Pro Ser Met Val Thr Asn Glu Gly Leu Gly Leu Thr
 850 855 860
 Thr Thr Ala Ser Gly Thr Asp Ile Ser Ser Asn Ser Leu Lys Asp Cys
 865 870 875 880
 Leu Pro Lys Ser Ala Gln Leu Leu Lys Ser Val Phe Val Lys Asn Val
 885 890 895
 Gly Trp Ala Thr Gln Leu Thr Ser Gly Ala Val Trp Val Gln Phe Asn
 900 905 910
 Asp Gly Ser Gln Leu Val Val Gln Ala Gly Val Ser Ser Ile Ser Tyr
 915 920 925
 Thr Ser Pro Asn Gly Gln Thr Thr Arg Tyr Gly Glu Asn Glu Lys Leu
 930 935 940
 Pro Asp Tyr Ile Lys Gln Lys Leu Gln Cys Leu Ser Ser Ile Leu Leu
 945 950 955 960
 Met Phe Ser Asn Pro Thr Pro Asn Phe His
 965 970

<210> 3
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(379)
 <223> SAK serine/threonine kinase kinase domain

<400> 3
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 20 25 30
 His Thr Gly Leu Glu Val Ala Ile Lys Met Ile Asp Lys Lys Ala Met
 35 40 45
 Tyr Lys Ala Gly Met Val Gln Arg Val Gln Asn Glu Val Lys Ile His
 50 55 60
 Cys Gln Leu Lys His Pro Ser Ile Leu Glu Leu Tyr Asn Tyr Phe Glu
 65 70 75 80
 Asp Ser Asn Tyr Val Tyr Leu Val Leu Glu Met Cys His Asn Gly Glu
 85 90 95
 Met Asn Arg Tyr Leu Lys Asn Arg Val Lys Pro Phe Ser Glu Asn Glu
 100 105 110
 Ala Arg His Phe Met His Gln Ile Ile Thr Gly Met Leu Tyr Leu His
 115 120 125
 Ser His Gly Ile Leu His Arg Asp Leu Thr Leu Ser Asn Leu Leu Leu
 130 135 140
 Thr Arg Asn Met Asn Ile Lys Ile Ala Asp Phe Gly Leu Ala Thr Gln
 145 150 155 160
 Leu Lys Met Pro His Glu Lys His Tyr Thr Leu Cys Gly Thr Pro Asn
 165 170 175
 Tyr Ile Ser Pro Glu Ile Ala Thr Arg Ser Ala His Gly Leu Glu Ser
 180 185 190
 Asp Val Trp Ser Leu Gly Cys Met Phe Tyr Thr Leu Leu Ile Gly Arg
 195 200 205
 Pro Pro Phe Asp Thr Asp Thr Val Lys Asn Thr Leu Asn Lys Val Val
 210 215 220
 Leu Ala Asp Tyr Glu Met Pro Ser Phe Leu Ser Ile Glu Ala Lys Asp
 225 230 235 240
 Leu Ile His Gln Leu Leu Arg Arg Asn Pro Ala Asp Arg Leu Ser Leu
 245 250 255
 Ser Ser Val Leu Asp His Pro Phe Met Ser Arg Asn Ser Ser Thr Lys
 260 265 270
 Ser Lys Asp Leu Gly Thr Val Glu Asp Ser Ile Asp Ser Gly His Ala
 275 280 285
 Thr Ile Ser Thr Ala Ile Thr Ala Ser Ser Ser Thr Ser Ile Ser Gly
 290 295 300
 Ser Leu Phe Asp Lys Arg Arg Leu Leu Ile Gly Gln Pro Leu Pro Asn
 305 310 315 320
 Lys Met Thr Val Phe Pro Lys Asn Lys Ser Ser Thr Asp Phe Ser Ser
 325 330 335
 Ser Gly Asp Gly Asn Ser Phe Tyr Thr Gln Trp Gly Asn Gln Glu Thr
 340 345 350
 Ser Asn Ser Gly Arg Gly Arg Val Ile Gln Asp Ala Glu Glu Arg Pro
 355 360 365
 His Ser Arg Tyr Leu Arg Arg Ala Tyr Ser Ser
 370 375

<210> 4
 <211> 373
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(373)
 <223> human FNK mitotic kinase kinase domain

<400> 4
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 1 5 10 15
 Ala Ala Ala Thr Ala Pro Pro Ala Gly Pro Gly Pro Pro Pro Ser Ala
 20 25 30
 Leu Arg Gly Pro Glu Leu Glu Met Leu Ala Gly Leu Pro Thr Ser Asp
 35 40 45
 Pro Gly Arg Leu Ile Thr Asp Pro Arg Ser Gly Arg Thr Tyr Leu Lys
 50 55 60
 Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr Glu Ala Thr
 65 70 75 80
 Asp Thr Glu Thr Gly Ser Ala Tyr Ala Val Lys Val Ile Pro Gln Ser
 85 90 95
 Arg Val Val Lys Pro His Gln Arg Glu Lys Ile Leu Asn Glu Ile Glu
 100 105 110
 Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe Ser His His
 115 120 125
 Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu Cys Ser Arg
 130 135 140
 Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu Leu Glu Pro
 145 150 155 160
 Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu Lys Tyr Leu
 165 170 175
 His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly Asn Phe Phe
 180 185 190
 Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly Leu Ala Ala
 195 200 205
 Arg Leu Glu Pro Pro Glu Gln Arg Lys Lys Thr Ile Cys Gly Thr Pro
 210 215 220
 Asn Tyr Val Ala Pro Glu Val Leu Leu Arg Gln Gly His Gly Pro Glu
 225 230 235 240
 Ala Asp Val Trp Ser Leu Gly Cys Val Met Tyr Thr Leu Leu Cys Gly
 245 250 255
 Ser Pro Pro Phe Glu Thr Ala Asp Leu Lys Glu Thr Tyr Arg Cys Ile
 260 265 270
 Lys Gln Val His Tyr Thr Leu Pro Ala Ser Leu Ser Leu Pro Ala Arg
 275 280 285
 Gln Leu Leu Ala Ala Ile Leu Arg Ala Ser Pro Arg Asp Arg Pro Ser
 290 295 300
 Ile Asp Gln Ile Leu Arg His Asp Phe Phe Thr Lys Gly Tyr Thr Pro
 305 310 315 320
 Asp Arg Leu Pro Ile Ser Ser Cys Val Thr Val Pro Asp Leu Thr Pro
 325 330 335
 Pro Asn Pro Ala Arg Ser Leu Phe Ala Lys Val Thr Lys Ser Leu Phe
 340 345 350
 Val Arg Lys Lys Lys Ser Lys Asn His Ala Gln Glu Arg Asp Glu Val
 355 360 365
 Ser Gly Leu Val Ser
 370

<210> 5
 <211> 400
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(400)
 <223> human SNK mitotic kinase kinase domain

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 20 25 30
 Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
 35 40 45
 Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
 50 55 60
 Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 65 70 75 80
 Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
 85 90 95
 Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 100 105 110
 Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
 115 120 125
 Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 130 135 140
 Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 145 150 155 160
 Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 165 170 175
 Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 180 185 190
 Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
 195 200 205
 Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
 210 215 220
 Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
 225 230 235 240
 Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
 245 250 255
 His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
 260 265 270
 Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
 275 280 285
 Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
 290 295 300
 Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
 305 310 315 320
 Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
 325 330 335
 Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
 340 345 350
 Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
 355 360 365
 Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
 370 375 380
 His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
 385 390 395 400

<210> 6
 <211> 367
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(367)
 <223> human PLK1 mitotic kinase kinase domain

<400> 6
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 Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
 35 40 45
 Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
 50 55 60
 Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
 65 70 75 80
 Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
 85 90 95
 Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
 100 105 110
 Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
 115 120 125
 Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg
 130 135 140
 Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
 145 150 155 160
 Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
 165 170 175
 Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
 180 185 190
 Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys
 195 200 205
 Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Ser
 210 215 220
 Lys Lys Gly His Ser Phe Glu Val Asp Val Trp Ser Ile Gly Cys Ile
 225 230 235 240
 Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser Cys Leu
 245 250 255
 Lys Glu Thr Tyr Leu Arg Ile Lys Lys Asn Glu Tyr Ser Ile Pro Lys
 260 265 270
 His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr
 275 280 285
 Asp Pro Thr Ala Arg Pro Thr Ile Asn Glu Leu Leu Asn Asp Glu Phe
 290 295 300
 Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr
 305 310 315 320
 Ile Pro Pro Arg Phe Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Asn
 325 330 335
 Arg Lys Pro Leu Thr Val Leu Asn Lys Gly Leu Glu Asn Pro Leu Pro
 340 345 350
 Glu Arg Pro Arg Glu Lys Glu Glu Pro Val Val Arg Glu Thr Gly
 355 360 365

<210> 7
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human ARK mitotic kinase

<400> 7

Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala Thr
1 5 10 15
Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Phe Pro
20 25 30
Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
35 40 45
Cys Pro Ser Asn Ser Ser Gln Arg Ile Pro Leu Gln Ala Gln Lys Leu
50 55 60
Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln
65 70 75 80
Gln Thr Ser Val Pro His Pro Val Ser Arg Pro Leu Asn Asn Thr Gln
85 90 95
Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
100 105 110
Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys Lys Arg Gln Trp
115 120 125
Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys Phe
130 135 140
Gly Asn Val Tyr Leu Ala Arg Glu Lys Gln Ser Lys Gly Ile Leu Ala
145 150 155 160
Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala Gly Val Glu His
165 170 175
Gln Leu Arg Arg Glu Val Glu Ile Gln Ser His Leu Arg His Pro Asn
180 185 190
Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr Arg Val Tyr Leu
195 200 205
Ile Leu Glu Tyr Ala Pro Leu Gly Thr Val Tyr Arg Glu Leu Gln Lys
210 215 220
Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr Ile Thr Glu Leu
225 230 235 240
Ala Asn Ala Leu Ser Tyr Cys His Ser Lys Arg Val Ile His Arg Asp
245 250 255
Ile Lys Pro Glu Asn Leu Leu Leu Gly Ser Ala Gly Glu Leu Lys Ile
260 265 270
Ala Asp Phe Gly Trp Ser Val His Ala Pro Ser Ser Arg Arg Thr Thr
275 280 285
Leu Cys Gly Thr Leu Asp Tyr Leu Pro Pro Glu Met Ile Glu Gly Arg
290 295 300
Met His Asp Glu Lys Val Asp Leu Trp Ser Leu Gly Val Leu Cys Tyr
305 310 315 320
Glu Phe Leu Val Gly Lys Pro Pro Phe Glu Ala Asn Thr Tyr Gln Glu
325 330 335
Thr Tyr Lys Arg Ile Ser Arg Val Glu Phe Thr Phe Pro Asp Phe Val
340 345 350
Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu Lys His Asn Pro
355 360 365
Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His Pro Trp Ile Thr
370 375 380
Ala Asn Ser Ser Lys Pro Ser Asn Cys Gln Asn Lys Glu Ser Ala Ser
385 390 395 400
Lys Gln Ser

<210> 8

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:flexible linker

<220>

<221> MOD_RES

<222> (6)..(200)

<223> Gly at positions 6-200 may be present or absent

<400> 8

A3
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
115 120 125
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145 150 155 160
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
165 170 175
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
180 185 190
Gly Gly Gly Gly Gly Gly Gly Gly
195 200